

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2002, 23:17:04 : Search time 77.62 Seconds
(without alignments)
5769.001 Million cell updates/sec

Title: US-09-909-567B-12
Perfect score: 1823
Sequence: 1 cccacttcgagagaccac.....aataattttaaaaaaa 1823

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 678.4 | 37.2 | 2061 | US-09-008-271A-16 | Sequence 16, Appl |
| 2 | 166.8 | 9.1 | 1800 | US-09-039-772A-1 | Sequence 1, Appl |
| 3 | 124 | 6.8 | 43676 | US-09-356-952-12 | Sequence 12, Appl |
| 4 | 117.2 | 6.4 | 1245 | US-09-318-443-1 | Sequence 1, Appl |
| 5 | 111.8 | 6.1 | 1682 | US-09-318-443-7 | Sequence 7, Appl |
| 6 | 108.6 | 6.0 | 1536 | US-09-318-443-5 | Sequence 5, Appl |
| 7 | 104.8 | 5.7 | 1374 | US-08-929-738-1 | Sequence 1, Appl |
| 8 | 104.8 | 5.7 | 1614 | US-08-929-738-2 | Sequence 2, Appl |
| 9 | 103.4 | 5.7 | 2365 | US-09-183-706-42 | Sequence 42, Appl |
| 10 | 103.4 | 5.7 | 2365 | US-09-567-995-42 | Sequence 42, Appl |
| 11 | 102 | 5.6 | 3825 | US-09-208-742-3 | Sequence 3, Appl |
| 12 | 84.4 | 4.6 | 1867 | US-08-607-509-3 | Sequence 3, Appl |
| 13 | 84.4 | 4.6 | 1867 | US-08-634-642-3 | Sequence 3, Appl |
| 14 | 84.4 | 4.6 | 1867 | US-08-989-370-3 | Sequence 3, Appl |
| 15 | 83.4 | 4.6 | 1618 | US-08-533-669A-9 | Sequence 9, Appl |
| 16 | 83.4 | 4.6 | 1618 | US-08-607-509-1 | Sequence 1, Appl |
| 17 | 83.4 | 4.6 | 1618 | US-08-454-036-1 | Sequence 1, Appl |
| 18 | 83.4 | 4.6 | 1618 | US-08-634-642-1 | Sequence 1, Appl |
| 19 | 83.4 | 4.6 | 1618 | US-08-989-370-1 | Sequence 1, Appl |
| 20 | 83.4 | 4.6 | 1618 | PCT-US95-05064-1 | Sequence 1, Appl |
| 21 | 75.4 | 4.1 | 3408 | US-09-058-489-14 | Sequence 14, Appl |
| 22 | 75.4 | 4.1 | 5322 | US-09-058-489-13 | Sequence 13, Appl |
| 23 | 70 | 3.8 | 2319 | US-09-058-489-90 | Sequence 90, Appl |
| 24 | 68.6 | 3.8 | 4416 | US-09-058-489-17 | Sequence 17, Appl |
| 25 | 68.6 | 3.8 | 700 | US-08-998-416-1131 | Sequence 1131, App |
| 26 | 68.6 | 3.8 | 1254 | PCT-US96-05320A-894 | Sequence 894, App |
| 27 | 67.4 | 3.7 | 2286 | US-09-176-657-4 | Sequence 4, Appl |

| | | | | | |
|----|------|-----|------|-------------------|-------------------|
| 28 | 66.2 | 3.6 | 1347 | US-08-959-749-1 | Sequence 1, Appl |
| 29 | 66.2 | 3.6 | 1347 | US-09-351-497-1 | Sequence 1, Appl |
| 30 | 62.2 | 3.4 | 2934 | US-09-149-934-2 | Sequence 2, Appl |
| 31 | 62.2 | 3.4 | 7218 | US-08-232-463-14 | Sequence 14, Appl |
| 32 | 57.6 | 3.2 | 532 | US-09-318-443-3 | Sequence 3, Appl |
| 33 | 51.4 | 2.8 | 672 | US-09-328-111-435 | Sequence 435, App |
| 34 | 50.8 | 2.8 | 342 | US-08-245-511-17 | Sequence 17, Appl |
| 35 | 50.8 | 2.8 | 1656 | US-08-600-993A-17 | Sequence 1, Appl |
| 36 | 48.6 | 2.7 | 1552 | US-09-503-391-3 | Sequence 3, Appl |
| 37 | 45.4 | 2.5 | 1997 | US-09-328-111-439 | Sequence 19, Appl |
| 38 | 45.2 | 2.5 | 470 | US-08-245-511-19 | Sequence 19, Appl |
| 39 | 43.8 | 2.4 | 235 | US-08-600-993A-19 | Sequence 19, Appl |
| 40 | 43.8 | 2.4 | 235 | US-08-328-111-478 | Sequence 478, App |
| 41 | 41.4 | 2.3 | 419 | US-09-007-005-17 | Sequence 17, Appl |
| 42 | 38.2 | 2.1 | 289 | US-09-244-796-17 | Sequence 17, Appl |
| 43 | 38.2 | 2.1 | 1560 | PCT-US94-09789-1 | Sequence 1, Appl |
| 44 | 37.2 | 2.0 | 1560 | US-09-009-443-1 | Sequence 1, Appl |
| 45 | 36.2 | 2.0 | 1676 | US-09-009-443-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-008-271A-16
Sequence 16, Application US/09008271A
Patent No. 6203979

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
Hillman, Jennifer L.

Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGST01
CLONE: 877617
SEQUENCE DESCRIPTION: SEQ ID NO: 16 :
US-09-008-271A-16

| | | | |
|----|------|--|------|
| OY | 518 | cttgaagcttcctaatactctgylcaagaa | 60 |
| Db | 1 | CTTGAGAGGCTCAATAACTTGGTCAAGAGAACCGAACCGAATCTGAATATGGAATTT | 637 |
| OY | 578 | tgaaacagaggttgtaaaagaatcctcaagtgatgtatccctcgagatcggaaaaacttccctt | 697 |
| Db | 61 | TGAACACGAGGTTGACAAG-----CTTCGAGATCGGAAAACAATTCCTCTT | 757 |
| OY | 638 | ctctgcaccaatgaccaagaaggttcataaacttcagtagagacgctcttgaaagatccigt | 165 |
| Db | 106 | CTCTGCCACCATGACCAAGAGGTTCAAAACCTTCAGGACGACACTCTGTAAGAAATCTCT | 165 |
| OY | 698 | gaatgtagcgttcctcctaataaccagaagcttgaaatathacgaatattatit | 225 |
| Db | 166 | GAAATGTGCGCTTTCCTTAATACCAAGACGTTGAAAATATACGCAATTTATTTT | 285 |
| OY | 758 | tattcccttaaatcaagaatacctaactggtttatatcttcaatgaatgctgtgaaa | 817 |
| Db | 226 | TATTCCTCTAATTAATTCAGAGTACTACTCGGTTATATCTTAATGAATGGCTGGAAA | 877 |
| OY | 818 | ctcccttaataatactctgcagagactctgtaataataaccagaagaacgcttgctactgcg | 345 |
| Db | 286 | CTCCTTATATATTTCTGCAGACCTGTAAATAATACCAAGAGAACGCTTCTACTCG | 405 |
| OY | 878 | aaactctgggttaactgcgcatccctccatgagacaatgaagcaagtaagcgctcag | 937 |
| Db | 346 | AAATCTTGCTTACAGTCGCATCCCTCTCATGAGAAATGTGATCAGATGAGGGCTTAG | 997 |
| OY | 938 | atcccttaataagtttaagggccaagcccggtccatcttcttaagcaatgaagcttgccag | 465 |
| Db | 406 | ATCCCTAATAAGTTTAAAGCCAAAGGCCGCTTCATTTCTTACAGTACGACGTGTCCAG | 1057 |
| OY | 998 | cggaggttgacatacctaactgatgtagtgtgtcaacttgacatcccttaaccatc | 525 |
| Db | 466 | CCGAGGTTTGACATACCTCATGTAGATGTGGTTGTCAACTTTGACATTCCTACCCTATC | 1117 |
| OY | 1058 | caagagatacatcatcgagtagtgtaaacagctctagagcttggtgcgctccggaaaggtat | 585 |
| Db | 526 | CAAGGATTAATCAATCCATCGATGATGGTCAACACGTAGAGGCTGGCGGAAAGGCTAT | 1177 |
| OY | 1118 | tactttgtacacagatgatagtgtgaaactctccagcgatatagaacacttaattggaa | 645 |
| Db | 586 | TACTTTGTACACACTATGATGTGAACTCTTCCACGCTATGAACACTTAATTGGGAA | 1237 |
| OY | 1178 | gaactacacaggttttccaacacagatgataaggtatagatgtgacagaacgctgcg | 705 |
| Db | 646 | GAACTACCAAGGTTTCCAAACACAGATCATAGGTTATGATGTGTGACAAACGCGTCCC | |

US-09-039-773A-1
Sequence 1 Application US/09039773A

Sequence: 6100388
Patent No. 6100388
GENERAL INFORMATION:
APPLICANT: Casas, Ivan
APPLICANT: Jonsson, Hans
APPLICANT: Wollstam, Bo
APPLICANT: Roos, Stefan
TITLE OF INVENTION: Lactobacilli Harboring Aggregation and Mucin
Binding Genes As Vaccine Delivery Vehicles
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Standley & Gilcrest
STREET: 495 Metro Place South, Suite 210
CITY: Dublin
STATE: Ohio
COUNTRY: US

ZIP: 43017
COMPUTER READABLE FORM: Diskette, 3.5 inch, 1.44MB storage
MEDIUM TYPE: IBM Compatible
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS Version 6.22
SOFTWARE: Microsoft Word Version 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,773A
FILING DATE: 16-MAR-1998
CLASSIFICATION: 536
PRIORITY INFORMATION: DATA: No. 6100388 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Donald O. Nickey
REGISTRATION NUMBER: 29,092
REFERENCE NUMBER: 1229-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614) 792-5555
TELEFAX: (614) 792-5536
TELEX: No. 6100388 applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
DESCRIPTION: Genomic DNA sequence and deduced
DESCRIPTION: acid sequence of bacterial aggre
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: Yes
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Lactobacillus reuteri sp
CELL TYPE: Unicellular organism
US-09-039-773A-1

| Query Match | Score | DB | Length |
|---------------------------|-------|------------|-----------------------|
| Best Local Similarity | 166.8 | 3 | 1800 |
| Matches 514; Conservative | 47.98 | | |
| | 0 | Mismatches | 557; Indels 3; Gaps 1 |

| | | | |
|----|-----|---|-----|
| QY | 102 | tttaagacccctggtgtgacagatgtgtgtgtgtgtgaagcttctgtgacagcttggagagctt | 246 |
| Db | 187 | ttttagctatttagcctttttccgattacccttatttttttttttttttttttttttttttttt | 221 |
| QY | 162 | aaaccaccacaagatccagattgaagcatctctcttggccctctcaagatctgagatcatcc | 306 |
| Db | 247 | GAAGCAACACCAATTCAGAAACAAACAGCATTCGAAATGCTTCTTGAGAGGTAGAGATGTTATT | 281 |
| QY | 222 | gggcttgcagaactcgcctctgcaaaagacagcgcttgccttgccttggcttggccattcaagca | 366 |
| Db | 307 | GGTCAAGCAACACTGGACACTGGTAAGCGGCTGCTTGGGTTGGCAATTTTGTAAAC | 426 |
| QY | 282 | ctgcctgagaccgcgcagagttgtttgttgcctagttcttaccgcagctcggagctgcgc | 401 |
| Db | 367 | GTTCATACCTGAAATATCCATATATTCACCAATTTATCATTTCCACCAACAGTGATATTAGCG | 486 |
| QY | 342 | tttcagatctcagagcaagtttgaagccctcgagctcctctatcttgagtgcagagttgctg | 461 |
| Db | 427 | ATCCAGACCCAGACAGACACTTTATGCTCTAGTAAAGATTAACATCTGTCCGTCGACAGTA | 506 |
| QY | 402 | attgtagtgtaattgatattaaatgctcaatcttgcgccttgaataaaataaccacatata | 546 |
| Db | 487 | GTCATATGTTGGGCGAGATATTCGGGCCCAATTAAGAGCTGTGAACACACACCCCAATTT | 521 |
| QY | 462 | ataatagcaactcctcgtgcgtctgattgacaccttggaaatacgaagaagtttcaacttg | 603 |
| Db | 547 | CTCGTGGGAGACCCCGAGACGCTTACGTGACGACCAATTAACCGTCATATACG---TTAAACTT | 588 |
| QY | 522 | agagctctcaactacttgatagtgtgtgaagccgaccgataactgatatgtatttgag | 603 |